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POS0741 **HISTOPATHOLOGIC PATTERNS OF LUPUS NEPHRITIS PREDICT THE RISKS OF MORTALITY. A SINGLE-CENTER RETROSPECTIVE STUDY**

Y. W. Liao¹, W. T. Hung¹, Y. M. Chen¹, C. W. Hsieh¹, T. Y. Hsieh¹, Y. H. Chen¹, W. N. Huang¹. ¹Taichung Veterans General Hospital, Division of Allergy, Immunology and Rheumatology, Taichung, Taiwan, Republic of China

Background: Lupus nephritis is a significant complication of systemic lupus erythematosus and is associated with increased risks of end-stage kidney disease and mortality.

Objectives: The retrospective observational study aims to investigate which component of the National Institutes of Health activity and chronic indices of lupus nephritis can predict mortality.

Methods: We identified 528 SLE patients with biopsy-proven lupus nephritis between 2006 and 2019. Two patients with class VI lupus nephritis were excluded, and a total of 526 patients were analyzed. Serum creatinine, urine protein-to-creatinine ratio (UPCR), and serologic markers for SLE disease activity were measured at the time of the renal biopsy. The histopathologic findings of renal biopsies were classified by utilizing the International Society of Nephrology/Renal Pathology Society (ISN/RPS) classification.

Results: Among 526 patients enrolled, 64 expired, and 44 were female (68.8%, p=0.004). Class IV (± V) comprised the most (n= 39, 60.9%), followed by class V (n= 18, 29.7%). Lower eGFR was observed in the death group, compared with the survival group (median: 24.7 vs. 80.5, p<0.001). There were no significant differences in UPCR and serologic markers for SLE (dsDNA, C3, and C4). Total scores of chronicity index and the scores for each index were higher in the death group. Interestingly, although total scores of activity index in death and survival groups did not differ significantly, the scores for cellular crescents tended to be higher in the death group (1.38 ±1.77 vs. 0.72 ±1.24, p=0.002).

In the univariable analysis, age, male sex, eGFR, activity index scores, cellular crescents, chronicity index scores, and all CI components (global obsolete glomeruli, tubular atrophy, interstitial fibrosis, fibrous crescents) and tubulointerstitial nephritis were significantly associated with an increased risk of death. When patient characteristics and NIH activity/ chronicity indices were jointly examined in a multivariable analysis, fibrous crescents were significantly associated with increased risk of death in females (HR 5.23 [95% CI: 1.51, 18.09]) (Table 1). In males, the risks of death increased with cellular crescents (HR 1.73 [95% CI: 1.10, 2.73]) but decreased with global obsolete glomeruli (HR 0.12 [95% CI: 0.02, 0.91]).

Conclusion: In this single-center observational study, fibrous crescents in females and cellular crescents in males were significantly associated with increased risks of mortality.

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POS0742 **SCREENING AND BIOINFORMATICS ANALYSIS OF HUB GENES AND PATHWAYS FOR PRIMARY SJÖGREN'S SYNDROME BASED ON GEO DATABASE**

T. Kong¹, S. X. Zhang^{2,3,4}, S. Song^{2,3,4}, X. Sun¹, C. Zheng¹, S. Feng⁵, L. Cheng¹, G. Shi⁶, X. Li^{2,3,4}, P. F. He⁷, Q. Yu^{1,7}. ¹Shanxi Medical University, School of Management, Taiyuan, China; ²The Second Hospital of Shanxi Medical University, Department of Rheumatology, Taiyuan, China; ³Shanxi Li Xiaofeng Medical Groups, Department of Rheumatology, Taiyuan, China; ⁴Ministry of Education, Key Laboratory of Cellular Physiology at Shanxi Medical University, Taiyuan, China; ⁵Shanxi Medical University, School of Humanities and Social Sciences, Taiyuan, China; ⁶Shanxi Medical University, Basic Medical College, Taiyuan, China; ⁷Shanxi Medical University, Institute of Medical Data Sciences, Taiyuan, China

Background: Primary Sjögren's syndrome (pSS) is an autoimmune disease that featured as lymphoplasmacytic infiltration of the exocrine glands leading to sicca symptoms¹. However, its underlying molecular mechanisms remain elusive.

Objectives: This study aims to identify differentially expressed genes (DEGs) and pathways associated with the progression of pSS using bioinformatics analysis and explore its pathogenesis.

Methods: The pSS-associated gene chip data set GSE66795 was obtained from the Gene Expression Omnibus (GEO) database, which included 131 cases of fully-phenotyped pSS patients' whole blood samples and 29 cases of control samples. DEGs were screened Using R software. Online tool Metascape² was used to make Gene Ontology (GO) and KEGG pathway enrichment. The PPI network was performed using String database. Hub genes were identified by Cytoscape.

Results: A total of 108 DEGs were captured, including 101 up-regulated genes and 7 down-regulated genes. GO enrichment showed that these DEGs were primarily enriched in defense response to virus, response to interferon-gamma, regulation of innate immune response, response to interferon-beta, double-stranded RNA binding, response to interferon-alpha. KEGG pathway enrichment analysis showed these DEGs were principally enriched in Influenza A, RIG-I-like receptor signaling pathway, necroptosis, Staphylococcus aureus infection. Finally, 9 hub genes (STAT1, IRF7, OAS2, GBP1, OAS1, IFIT3, IFIH1, OAS3, DDX60) had highest degree value.

Conclusion: The findings identified molecular mechanisms and the key hub genes that may involve in the occurrence and development of pSS.

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Table 1. Logistic regression of predictors for mortality in patients with lupus nephritis

	Univariable			Multivariable (Female)			Multivariable (Male)		
	HR	95% CI	p value	HR	95% CI	p value	HR	95% CI	p value
Age	1.03	(1.01-1.05)	0.002	1.02	(0.98-1.07)	0.267	1.01	(0.95-1.08)	0.670
Male sex	2.10	(1.23-3.55)	0.006						
UPCR	1.02	(0.95-1.09)	0.616						
eGFR	0.97	(0.96-0.99)	<0.001	0.99	(0.96-1.00)	0.183	0.98	(0.96-1.00)	0.086
Activity Index	1.06	(1.01-1.11)	0.027						
Cellular crescents	1.29	(1.12-1.50)	<0.001	1.03	(0.63-1.67)	0.917	1.73	(1.10-2.73)	0.017
Chronicity Index	1.16	(1.07-1.26)	<0.001						
global obsolete glomeruli	1.37	(1.08-1.76)	0.011	1.24	(0.55-2.77)	0.606	0.12	(0.02-0.91)	0.040
Tubular atrophy	1.65	(1.28-2.13)	<0.001	0.41	(0.06-2.82)	0.362	4.77	(0.30-75.32)	0.267
Interstitial fibrosis	1.71	(1.32-2.23)	<0.001	3.70	(0.52-26.24)	0.191	1.37	(0.07-27.40)	0.837
Fibrous crescents	2.38	(1.40-4.03)	0.001	5.23	(1.51-18.09)	0.009	0.00	(0-extremely large)	0.989
Tubulointerstitial nephritis	1.70	(1.03-2.80)	0.037						